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Sequence Listing was accepted with existing errors.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: Mon Jun 25 16:59:13 EDT 2007

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Application No: 10541947 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2007-06-21 10:13:26.687  
**Finished:** 2007-06-21 10:13:27.311  
**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 624 ms  
**Total Warnings:** 0  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 9  
**Actual SeqID Count:** 9

Error code	Error Description
E 300	Invalid codon found acg SEQID (5) POS: 175

## SEQUENCE LISTING

<110> North Carolina State University  
Petitte, James  
Pardue, Samuel

<120> DEPLETION OF ENDOGENOUS PRIMORDIAL GERM CELLS IN AVIAN SPECIES

<130> 297/204 PCT

<140> 10541947

<141> 2005-12-12

<150> US 60/440,424

<151> 2003-01-16

<160> 9

<170> PatentIn version 3.2

<210> 1

<211> 1989

<212> DNA

<213> Gallus gallus

<220>

<221> CDS

<222> (1)..(1989)

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tcc cag ggg cgt tct gag gag cag gcg tgg atg gct aac tct ggc aga       96  
Ser Gln Gly Arg Ser Glu Glu Gln Ala Trp Met Ala Asn Ser Gly Arg  
20               25               30

cca aac agc cca tcc ctc cgc ttc tcc agc aga cca agc agc ccc ttg      144  
Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu  
35               40               45

tct ggc ttc cca ggc aga cca aac agc ccc ttc ttt ggc ttt agt cag      192  
Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln  
50               55               60

aat aaa ggc tca ctt ggt gct aat gaa gga ctt aac aga agt ctg cct      240  
Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro  
65               70               75               80

gtg cag cat gac att gga gga tat tct ggg agc aga gag tct gtt gta      288  
Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val  
85               90               95

cgt caa aac aga gaa gat caa cca gtg act aga ttt ggt aga ggg agg      336  
Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg

100	105	110	
agt tct gga agc aga gat ttt caa gag agg aac tct gca aat gat cct			384
Ser Ser Gly Ser Arg Asp Phe Gln Glu Arg Asn Ser Ala Asn Asp Pro			
115	120	125	
ggt atg caa gat caa ggt ttt aga aga gtt cct ggc atc ttt ggg caa			432
Gly Met Gln Asp Gln Gly Phe Arg Arg Val Pro Gly Ile Phe Gly Gln			
130	135	140	
agc aag tgt ttt aac agt gag gaa aga aat agt cct ctg cgt ggc agc			480
Ser Lys Cys Phe Asn Ser Glu Glu Arg Asn Ser Pro Leu Arg Gly Ser			
145	150	155	160
cct ttt gcc cca gga gga aga gca gtt gga ggt cct gca gga gtt			528
Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val			
165	170	175	
ctc aaa gga cgc tct gaa gaa att gat tct gga aga ggt cca aag gtg			576
Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val			
180	185	190	
act tat gtc ccc cct cct cca cct gaa gat gaa cag tcc atc ttt gca			624
Thr Tyr Val Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala			
195	200	205	
tgt tat cag tca gga att aat ttt gac aag tat gat gaa tgt gct gtt			672
Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val			
210	215	220	
gag atg tca gga ctt gac cct cca gca cca tta ctg gct ttt gaa gaa			720
Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu			
225	230	235	240
gct aac ttt gct cag act tta agg aag aat ata tct aaa act gga tat			768
Ala Asn Phe Ala Gln Thr Leu Arg Lys Asn Ile Ser Lys Thr Gly Tyr			
245	250	255	
tca aaa ctt act cca gtg cag aag cac agc att cct gtt ata caa gca			816
Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala			
260	265	270	
ggg cgg gat tta atg tca tgt gcc cag aca gga tca gga aaa aca gca			864
Gly Arg Asp Leu Met Ser Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala			
275	280	285	
gct ttt ctt cta cca att gtg gac cgg atg atg aaa gat ggt gta act			912
Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr			
290	295	300	
gca agc ttc cca aag cag caa gac cca caa tgc att att gtt gca cca			960
Ala Ser Phe Pro Lys Gln Gln Asp Pro Gln Cys Ile Ile Val Ala Pro			
305	310	315	320
act aga gaa ctg ata aat cag atc ttc tta gaa gca agg aag ttt gtg			1008
Thr Arg Glu Leu Ile Asn Gln Ile Phe Leu Glu Ala Arg Lys Phe Val			
325	330	335	

tat	ggg	act	tgt	ata	agg	cct	gtt	gtg	atc	tat	gga	ggt	aca	cag	aca	1056
Tyr	Gly	Thr	Cys	Ile	Arg	Pro	Val	Val	Ile	Tyr	Gly	Gly	Thr	Gln	Thr	
				340			345			350						
ggt	cat	tca	atc	cgt	caa	ata	atg	caa	ggc	tgt	aat	ata	tta	tgt	gcc	1104
Gly	His	Ser	Ile	Arg	Gln	Ile	Met	Gln	Gly	Cys	Asn	Ile	Leu	Cys	Ala	
				355			360			365						
act	cct	gga	agg	ctt	ctt	gac	att	att	gaa	aaa	ggg	aag	atc	agt	ttg	1152
Thr	Pro	Gly	Arg	Leu	Leu	Asp	Ile	Ile	Glu	Lys	Gly	Lys	Ile	Ser	Leu	
				370			375			380						
gtg	gag	gtg	aaa	tat	ttg	gta	cta	gat	gaa	gca	gac	cgc	atg	ctc	gat	1200
Val	Glu	Val	Lys	Tyr	Leu	Val	Leu	Asp	Glu	Ala	Asp	Arg	Met	Leu	Asp	
				385			390			395			400			
atg	ggt	ttt	gga	tta	gat	atg	aag	aag	ctg	att	tct	tat	cca	gaa	atg	1248
Met	Gly	Phe	Gly	Leu	Asp	Met	Lys	Lys	Leu	Ile	Ser	Tyr	Pro	Glu	Met	
				405			410			415						
cca	tct	aaa	gac	aga	cgt	caa	aca	tta	atg	ttt	agt	gcc	act	ttt	cct	1296
Pro	Ser	Lys	Asp	Arg	Arg	Gln	Thr	Leu	Met	Phe	Ser	Ala	Thr	Phe	Pro	
				420			425			430						
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Glu	Glu	Val	Gln	Arg	Leu	Ala	Gly	Glu	Phe	Leu	Lys	Thr	Asp	Tyr	Ile	
				435			440			445						
ttt	ctt	gtt	att	gga	aat	acc	tgt	gga	gcc	tgc	agt	gat	gtt	cag	caa	1392
Phe	Leu	Val	Ile	Gly	Asn	Thr	Cys	Gly	Ala	Cys	Ser	Asp	Val	Gln	Gln	
				450			455			460						
aat	att	ctt	cag	gtt	ccc	cgg	tta	tcc	aag	agg	gat	aaa	cta	ata	gaa	1440
Asn	Ile	Leu	Gln	Val	Pro	Arg	Leu	Ser	Lys	Arg	Asp	Lys	Leu	Ile	Glu	
				465			470			475			480			
att	cta	caa	agc	aca	ggt	ggt	gaa	cga	acc	atg	gtg	ttt	gtg	gac	aca	1488
Ile	Leu	Gln	Ser	Thr	Gly	Gly	Glu	Arg	Thr	Met	Val	Phe	Val	Asp	Thr	
				485			490			495						
aag	aaa	aaa	gca	gat	tac	ctt	gca	gcc	ttt	ctt	tgt	caa	gag	aac	cta	1536
Lys	Lys	Lys	Ala	Asp	Tyr	Leu	Ala	Ala	Phe	Leu	Cys	Gln	Glu	Asn	Leu	
				500			505			510						
cca	tcc	acc	agc	att	cat	gga	gat	agg	gaa	cag	aga	gag	aga	gag	ata	1584
Pro	Ser	Thr	Ser	Ile	His	Gly	Asp	Arg	Glu	Gln	Arg	Glu	Arg	Glu	Ile	
				515			520			525						
gct	ctt	cgc	gat	ttc	cgt	tct	gga	aaa	tgt	caa	att	ctt	gtg	gca	act	1632
Ala	Leu	Arg	Asp	Phe	Arg	Ser	Gly	Lys	Cys	Gln	Ile	Leu	Val	Ala	Thr	
				530			535			540						
tcg	gta	gca	tca	aga	ggc	ctg	gat	att	gaa	aat	gtt	caa	cat	gtt	att	1680
Ser	Val	Ala	Ser	Arg	Gly	Leu	Asp	Ile	Glu	Asn	Val	Gln	His	Val	Ile	
				545			550			555			560			

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Asn Phe Asp Leu Pro Asn Thr Ile Glu Asp Tyr Val His Arg Ile Gly			
565	570	575	
cga act ggt cgt tgt gga aat act ggc aaa gca gtt tca ttc ttt gat			1776
Arg Thr Gly Arg Cys Gly Asn Thr Gly Lys Ala Val Ser Phe Phe Asp			
580	585	590	
gat cag tca gat ggc cat ctt gta caa tca cta ctt aaa gtg ctt tcc			1824
Asp Gln Ser Asp Gly His Leu Val Gln Ser Leu Leu Lys Val Leu Ser			
595	600	605	
aga acc cag cag gaa ttc cag ttt ggt gga aga atg gct gtc caa aga			1872
Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg			
610	615	620	
aca aat att gtt gct tca act tgg tgc cca aag gga tta atg cag gcc			1920
Thr Asn Ile Val Ala Ser Thr Trp Cys Pro Lys Gly Leu Met Gln Ala			
625	630	635	640
gtg gca gaa tgg aac cca aga gaa atg agg atg tca tat tct gaa aca			1968
Val Ala Glu Trp Asn Pro Arg Glu Met Arg Met Ser Tyr Ser Glu Thr			
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Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu			
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Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln			
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Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro			
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Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val			

85

90

95

Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg  
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Ser Ser Gly Ser Arg Asp Phe Gln Glu Arg Asn Ser Ala Asn Asp Pro  
115 120 125

Gly Met Gln Asp Gln Gly Phe Arg Arg Val Pro Gly Ile Phe Gly Gln  
130 135 140

Ser Lys Cys Phe Asn Ser Glu Glu Arg Asn Ser Pro Leu Arg Gly Ser  
145 150 155 160

Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val  
165 170 175

Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val  
180 185 190

Thr Tyr Val Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala  
195 200 205

Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val  
210 215 220

Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu  
225 230 235 240

Ala Asn Phe Ala Gln Thr Leu Arg Lys Asn Ile Ser Lys Thr Gly Tyr  
245 250 255

Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala  
260 265 270

Gly Arg Asp Leu Met Ser Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala  
275 280 285

Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr  
290 295 300

Ala Ser Phe Pro Lys Gln Gln Asp Pro Gln Cys Ile Ile Val Ala Pro  
305 310 315 320

Thr Arg Glu Leu Ile Asn Gln Ile Phe Leu Glu Ala Arg Lys Phe Val  
325 330 335

Tyr Gly Thr Cys Ile Arg Pro Val Val Ile Tyr Gly Gly Thr Gln Thr  
340 345 350

Gly His Ser Ile Arg Gln Ile Met Gln Gly Cys Asn Ile Leu Cys Ala  
355 360 365

Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu  
370 375 380

Val Glu Val Lys Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp  
385 390 395 400

Met Gly Phe Gly Leu Asp Met Lys Lys Leu Ile Ser Tyr Pro Glu Met  
405 410 415

Pro Ser Lys Asp Arg Arg Gln Thr Leu Met Phe Ser Ala Thr Phe Pro  
420 425 430

Glu Glu Val Gln Arg Leu Ala Gly Glu Phe Leu Lys Thr Asp Tyr Ile  
435 440 445

Phe Leu Val Ile Gly Asn Thr Cys Gly Ala Cys Ser Asp Val Gln Gln  
450 455 460

Asn Ile Leu Gln Val Pro Arg Leu Ser Lys Arg Asp Lys Leu Ile Glu  
465 470 475 480

Ile Leu Gln Ser Thr Gly Gly Glu Arg Thr Met Val Phe Val Asp Thr  
485 490 495

Lys Lys Lys Ala Asp Tyr Leu Ala Ala Phe Leu Cys Gln Glu Asn Leu  
500 505 510

Pro Ser Thr Ser Ile His Gly Asp Arg Glu Gln Arg Glu Arg Glu Ile  
515 520 525

Ala Leu Arg Asp Phe Arg Ser Gly Lys Cys Gln Ile Leu Val Ala Thr  
530 535 540

Ser Val Ala Ser Arg Gly Leu Asp Ile Glu Asn Val Gln His Val Ile  
545 550 555 560

Asn Phe Asp Leu Pro Asn Thr Ile Glu Asp Tyr Val His Arg Ile Gly  
565 570 575

Arg Thr Gly Arg Cys Gly Asn Thr Gly Lys Ala Val Ser Phe Phe Asp  
580 585 590

Asp Gln Ser Asp Gly His Leu Val Gln Ser Leu Leu Lys Val Leu Ser  
595 600 605

Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg  
610 615 620

Thr Asn Ile Val Ala Ser Thr Trp Cys Pro Lys Gly Leu Met Gln Ala  
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gaaggcctcg tttgtttta agtgtgcggg cgctgtcaca gctccgggga acg atg 176

Met

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tct gca aat gcg gaa gcc cag tgt gga agt atc tca gag gat aat acc 224

Ser Ala Asn Ala Glu Ala Gln Cys Gly Ser Ile Ser Glu Asp Asn Thr

5

10

15

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His Ser Ser Thr Thr Cys Gln Gly Tyr Val Leu Pro Glu Gly Lys Ile

20

25

30

atg cca aat aca gtc ttt gtt ggt gga att gat ata agg atg aat gaa 320

Met Pro Asn Thr Val Phe Val Gly Gly Ile Asp Ile Arg Met Asn Glu

35

40

45

gca gaa att cgg agt tac ttt gaa caa tat ggt act gtg aag gag gtg 368

Ala Glu Ile Arg Ser Tyr Phe Glu Gln Tyr Gly Thr Val Lys Glu Val

50

55

60

65

aaa ata atc act gac aga act ggt gtt tcc aaa ggg tat gga ttt gtt 416

Lys Ile Ile Thr Asp Arg Thr Gly Val Ser Lys Gly Tyr Gly Phe Val

70

75

80

tca ttc ctg gac aat gtg gat gtt caa aag ata gta gaa tca cag atc 464

Ser Phe Leu Asp Asn Val Asp Val Gln Lys Ile Val Glu Ser Gln Ile

85